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Date of mailing (day/month/year) 18 May 2000 (18.05.00)	
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International filing date (day/month/year) 29 July 1999 (29.07.99)	Priority date (day/month/year) 29 July 1998 (29.07.98)
Applicant SIM, Gek-Kee et al	

1. The designated Office is hereby notified of its election made:

☒ in the demand filed with the International Preliminary Examining Authority on:
 29 February 2000 (29.02.00)

☐ in a notice effecting later election filed with the International Bureau on:

2. The election ☒ was
☐ was not

made before the expiration of 19 months from the priority date or, where Rule 32 applies, within the time limit under Rule 32.2(b).

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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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(21) International Application Number: PCT/US99/17309 (22) International Filing Date: 29 July 1999 (29.07.99) (30) Priority Data: 60/094,506 29 July 1998 (29.07.98) US (63) Related by Continuation (CON) or Continuation-in-Part (CIP) to Earlier Application US 60/094,506 (CIP) Filed on 29 July 1998 (29.07.98) (71) Applicant (for all designated States except US): HESKA CORPORATION [US/US]; 1825 Sharp Point Drive, Fort Collins, CO 80525 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): SIM, Gek-Kee [US/US]; 3622 Terry Point Drive, Fort Collins, CO 80524 (US). DREITZ, Matthew, J. [US/US]; 4324 Winterstone, Fort Collins, CO 80525 (US). (74) Agents: CONNELL, Gary, J. et al.; Sheridan Ross P.C., Suite 3500, 1700 Lincoln Street, Denver, CO 80203-4501 (US).		(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the international search report: 4 May 2000 (04.05.00)
(54) Title: T CELL RECEPTOR PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF (57) Abstract <p>The present invention relates to TCR Vβ proteins; to TCR Vβ nucleic acid molecules, including those that encode such TCR Vβ proteins; to antibodies raised against such TCR Vβ proteins; and to therapeutic compounds that regulate TCR Vβ function. The present invention also includes methods to identify and obtain such proteins, nucleic acid molecules, antibodies, and inhibitory compounds. Also included in the present invention are therapeutic compositions comprising such proteins, nucleic acid molecules, antibodies and/or inhibitory compounds as well as the use of such therapeutic compositions to regulate an immune response in an animal. Also included in the present invention are methods to detect T cell expansion in an animal using reagents including, or derived from such proteins, nucleic acid molecules or antibodies.</p>		

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SEQUENCE LISTING

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 Met Asn Ser Leu Glu Pro Gly Asp Ser Ala Leu Tyr Leu Cys Ala Ser
 100 105 110

agc tta gat gcg ttc gac gcg ggg cag ctg tac ttc ggg gcc ggt tcc 384
 Ser Leu Asp Ala Phe Asp Ala Gly Gln Leu Tyr Phe Gly Ala Gly Ser
 115 120 125

aag ctg gcc gtg ctg 399
 Lys Leu Ala Val Leu
 130

<210> 18

<211> 399

<212> DNA

<213> Canis familiaris

<400> 18

cagcacggcc agcttggaac cggccccgaa gtacagctgc cccgcgtcga acgcatctaa 60

gctgctggca cagagatata gggctgagtc tcttggtcc agggagtcca tctccagctg 120
 ggagctgtag ttactgaact gctgcactga gaatcttgcc gggatgtctc ctttgtctct 180

ctcttcctta ttgtaatact gaatgagaaa ccggggaccc tggcccaggg cctgttggtta 240

ccagtacaca gataggtgtc cagagataag ggaacatctc agggtcactg tctgtcctct 300
 tgctttgatc atgtgtcttg gagtttggat gacctcagac tccacggggc cggtccccag 360
 gagacaaagg gccacacagc agagaagcct ggagcccat 399

<210> 19
 <211> 462
 <212> DNA
 <213> Canis familiaris

<220>
 <221> CDS
 <222> (73)..(462)

<400> 19
 gctgcaggat tcggcacgag gcgtggatcat atctatcttg agagaggtat ggtatgaggc 60
 catcacctga ag atg ctg atg ctt ctg ctg ctc ctg ggg ccc agc tct gga 111
 Met Leu Met Leu Leu Leu Leu Leu Gly Pro Ser Ser Gly
 1 5 10
 ctc ggt gcc ctc gtc ttc cag gcg ccc agc aca atg atc tgt aag agc 159
 Leu Gly Ala Leu Val Phe Gln Ala Pro Ser Thr Met Ile Cys Lys Ser
 15 20 25
 gga gcc acc gtg cag atc cag tgt caa aca gtg gac ctt caa gcc aca 207
 Gly Ala Thr Val Gln Ile Gln Cys Gln Thr Val Asp Leu Gln Ala Thr
 30 35 40 45
 acc gtg ttt tgg tat cgc cag ctc ccg aag cag ggc ctt acc ctt atg 255
 Thr Val Phe Trp Tyr Arg Gln Leu Pro Lys Gln Gly Leu Thr Leu Met
 50 55 60
 gtg acc tct aac gtg ggc aac agt gct aca cac gag cag ggg ttc cct 303
 Val Thr Ser Asn Val Gly Asn Ser Ala Thr His Glu Gln Gly Phe Pro
 65 70 75
 gca gcc aag ttc cct gtt aac cac cca aac ctc acg ttt tcc tcc ctg 351
 Ala Ala Lys Phe Pro Val Asn His Pro Asn Leu Thr Phe Ser Ser Leu
 80 85 90
 atg gtg acg agt tca ggt cct gga gac agc ggc ctc tac ttc tgt ggt 399
 Met Val Thr Ser Ser Gly Pro Gly Asp Ser Gly Leu Tyr Phe Cys Gly
 95 100 105
 gtt cgg gcg tat ggt ggg aac tcg ccc ctc tac ttt gga aca ggc acc 447
 Val Arg Ala Tyr Gly Gly Asn Ser Pro Leu Tyr Phe Gly Thr Gly Thr
 110 115 120 125

agg ctc acc gtg aca
 Arg Leu Thr Val Thr
 130

462

<210> 20
 <211> 130
 <212> PRT
 <213> Canis familiaris

<400> 20

Met Leu Met Leu Leu Leu Leu Gly Pro Ser Ser Gly Leu Gly Ala
 1 5 10 15

Leu Val Phe Gln Ala Pro Ser Thr Met Ile Cys Lys Ser Gly Ala Thr
 20 25 30

Val Gln Ile Gln Cys Gln Thr Val Asp Leu Gln Ala Thr Thr Val Phe
 35 40 45

Trp Tyr Arg Gln Leu Pro Lys Gln Gly Leu Thr Leu Met Val Thr Ser
 50 55 60

Asn Val Gly Asn Ser Ala Thr His Glu Gln Gly Phe Pro Ala Ala Lys
 65 70 75 80

Phe Pro Val Asn His Pro Asn Leu Thr Phe Ser Ser Leu Met Val Thr
 85 90 95

Ser Ser Gly Pro Gly Asp Ser Gly Leu Tyr Phe Cys Gly Val Arg Ala
 100 105 110

Tyr Gly Gly Asn Ser Pro Leu Tyr Phe Gly Thr Gly Thr Arg Leu Thr
 115 120 125

Val Thr
 130

<210> 21
 <211> 462
 <212> DNA
 <213> Canis familiaris

<400> 21

tgtcacgggtg agcctgggtgc ctgttccaaa gtagagggggc gagttccac catacgcccg 60

aacaccacag aagtagaggc cgctgtctcc aggacctgaa ctggtcacca tcagggagga 120

aaacgtgagg tttgggtggt taacagggaa cttggctgca gggaaccct gctcgtgtgt 180
 agcactgttg cccacgttag aggtcaccat aagggttaagg ccttgcctcg ggagctggcg 240
 atacaaaaac acggttggtg cttgaaggtc cactgtttga cactggatct gcacgggtggc 300
 tccgctctta cagatcattg tgctgggccc ctggaagacg agggcaccga gtccagagct 360
 gggccccagg agcagcagaa gcacagcat cttcaggtga tggcctcata ccatacctct 420
 ctcaagatag atatgaccac gcctcgtgcc gaatcctgca gc 462

<210> 22

<211> 417

<212> DNA

<213> *Canis familiaris*

<220>

<221> CDS

<222> (13)..(417)

<400> 22

cacgagcctg cc atg tgc cca gtg ttc atc tgc tcc ttg gtc ctc tgg ctc 51
 Met Cys Pro Val Phe Ile Cys Ser Leu Val Leu Trp Leu
 1 5 10

ctg agt aca ggc acc ctc aat gca aaa gtc atg cag act cca gga cat 99
 Leu Ser Thr Gly Thr Leu Asn Ala Lys Val Met Gln Thr Pro Gly His
 15 20 25

ctg gtc aaa ggg aaa gga caa aaa gca aaa atg gaa tgt gtc cca ata 147
 Leu Val Lys Gly Lys Gly Gln Lys Ala Lys Met Glu Cys Val Pro Ile
 30 35 40 45

aaa gga cat agt tat gtt ttc tgg tat cag cag atc cca gca aaa gag 195
 Lys Gly His Ser Tyr Val Phe Trp Tyr Gln Gln Ile Pro Ala Lys Glu
 50 55 60

ttc aag ttc ttg att tct ttc cag gat aac gct gtc ttt gat aaa aca 243
 Phe Lys Phe Leu Ile Ser Phe Gln Asp Asn Ala Val Phe Asp Lys Thr
 65 70 75

ggg atg ccc acg cag aga ttt tta gcc ttg tgt cca aaa aac cta ccc 291
 Gly Met Pro Thr Gln Arg Phe Leu Ala Leu Cys Pro Lys Asn Leu Pro
 80 85 90

tgt agc cta gag atc gag cgt aca gag ctg cag gat tca gcc gtg tat 339
 Cys Ser Leu Glu Ile Glu Arg Thr Glu Leu Gln Asp Ser Ala Val Tyr
 95 100 105

ttt tgt gcc agc agt gac aga act ggg gga ctc gtt cac gag cag tat 387

Phe Cys Ala Ser Ser Asp Arg Thr Gly Gly Leu Val His Glu Gln Tyr
 110 115 120 125

ttc ggc gcc ggc acc agg ctc acg gtc ctc 417
 Phe Gly Ala Gly Thr Arg Leu Thr Val Leu
 130 135

<210> 23
 <211> 135
 <212> PRT
 <213> Canis familiaris

<400> 23
 Met Cys Pro Val Phe Ile Cys Ser Leu Val Leu Trp Leu Leu Ser Thr
 1 5 10 15

Gly Thr Leu Asn Ala Lys Val Met Gln Thr Pro Gly His Leu Val Lys
 20 25 30

Gly Lys Gly Gln Lys Ala Lys Met Glu Cys Val Pro Ile Lys Gly His
 35 40 45

Ser Tyr Val Phe Trp Tyr Gln Gln Ile Pro Ala Lys Glu Phe Lys Phe
 50 55 60

Leu Ile Ser Phe Gln Asp Asn Ala Val Phe Asp Lys Thr Gly Met Pro
 65 70 75 80

Thr Gln Arg Phe Leu Ala Leu Cys Pro Lys Asn Leu Pro Cys Ser Leu
 85 90 95

Glu Ile Glu Arg Thr Glu Leu Gln Asp Ser Ala Val Tyr Phe Cys Ala
 100 105 110

Ser Ser Asp Arg Thr Gly Gly Leu Val His Glu Gln Tyr Phe Gly Ala
 115 120 125

Gly Thr Arg Leu Thr Val Leu
 130 135

<210> 24
 <211> 417
 <212> DNA
 <213> Canis familiaris

<400> 24
 gaggaccgtg agcctggtgc cggcgccgaa atactgctcg tgaacgagtc cccagttct 60

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<210> 25
<211> 423
<212> DNA
<213> Canis familiaris
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<220>
<221> CDS
<222> (40) .. (423)
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<400> 25																	
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												1				5	
ctc	tgc	tgt	atg	gtc	ctc	tgc	ctc	ctg	gga	gca	gca	ccc	ctg	gac	aca	102	
Leu	Cys	Cys	Met	Val	Leu	Cys	Leu	Leu	Gly	Ala	Ala	Pro	Leu	Asp	Thr		
				10					15					20			
aca	gtt	tcc	cag	act	cca	aga	tac	ctc	atc	gcg	cac	gtg	gga	tcg	aag	150	
Thr	Val	Ser	Gln	Thr	Pro	Arg	Tyr	Leu	Ile	Ala	His	Val	Gly	Ser	Lys		
			25					30					35				
aag	tta	cta	aaa	tgt	gag	caa	aat	ctg	ggc	cat	aat	gct	atg	tac	tgg	198	
Lys	Leu	Leu	Lys	Cys	Glu	Gln	Asn	Leu	Gly	His	Asn	Ala	Met	Tyr	Trp		
		40					45					50					
tat	aag	caa	gac	ctc	aag	caa	ctg	ctg	aag	atc	atg	ttt	atc	tac	ttt	246	
Tyr	Lys	Gln	Asp	Leu	Lys	Gln	Leu	Leu	Lys	Ile	Met	Phe	Ile	Tyr	Phe		
	55					60				65							
aat	cag	gga	ctc	aat	cta	aat	gaa	tca	gtt	cca	ggt	cgt	ttc	tca	cct	294	
Asn	Gln	Gly	Leu	Asn	Leu	Asn	Glu	Ser	Val	Pro	Gly	Arg	Phe	Ser	Pro		
	70				75					80					85		
gag	aca	ctg	aca	agc	tca	tta	act	tca	tgt	cga	ctc	ctg	aac	agt	gac	342	
Glu	Thr	Leu	Thr	Ser	Ser	Leu	Thr	Ser	Cys	Arg	Leu	Leu	Asn	Ser	Asp		
				90					95					100			

tct gct gtg tat ttc tgt gcc agc agc gag ggg tat gat gaa aaa ttg 390
 Ser Ala Val Tyr Phe Cys Ala Ser Ser Glu Gly Tyr Asp Glu Lys Leu
 105 110 115

tat ttt gca agt gga acc aag ctt tct gtc ttg 423
 Tyr Phe Ala Ser Gly Thr Lys Leu Ser Val Leu
 120 125

<210> 26
 <211> 128
 <212> PRT
 <213> Canis familiaris

<400> 26
 Met Gly Ser Gly Phe Leu Cys Cys Met Val Leu Cys Leu Leu Gly Ala
 1 5 10 15

Ala Pro Leu Asp Thr Thr Val Ser Gln Thr Pro Arg Tyr Leu Ile Ala
 20 25 30

His Val Gly Ser Lys Lys Leu Leu Lys Cys Glu Gln Asn Leu Gly His
 35 40 45

Asn Ala Met Tyr Trp Tyr Lys Gln Asp Leu Lys Gln Leu Leu Lys Ile
 50 55 60

Met Phe Ile Tyr Phe Asn Gln Gly Leu Asn Leu Asn Glu Ser Val Pro
 65 70 75 80

Gly Arg Phe Ser Pro Glu Thr Leu Thr Ser Ser Leu Thr Ser Cys Arg
 85 90 95

Leu Leu Asn Ser Asp Ser Ala Val Tyr Phe Cys Ala Ser Ser Glu Gly
 100 105 110

Tyr Asp Glu Lys Leu Tyr Phe Ala Ser Gly Thr Lys Leu Ser Val Leu
 115 120 125

<210> 27
 <211> 423
 <212> DNA
 <213> Canis familiaris

<400> 27
 caagacagaa agcttggttc cacttgcaaa atacaatttt tcatcatacc cctcgctgct 60
 ggcacagaaa tacacagcag agtcactggt caggagtcga catgaagtta atgagcttgt 120
 cagtgtctca ggtgagaaac gacctggaac tgattcatTT agattgagtc cctgattaaa 180

gtagataaac atgatcttca gcagttgctt gaggtcttgc ttataccagt acatagcatt 240
 atggcccaga ttttgctcac attttagtaa cttcttcgat cccacgtgcg cgatgaggta 300
 tcttggagtc tgggaaactg ttgtgtccag ggggtgctgct cccaggaggc agaggacccat 360
 acagcagagg aaccgggagc ccatggtgga gacaggcaca gtctggctct cagtgtctcg 420
 gcc 423

<210> 28
 <211> 333
 <212> DNA
 <213> Canis familiaris

<220>
 <221> CDS
 <222> (1)..(333)

<400> 28
 atc gga ctc ctc tgt ggt gtg gcc ttt tgt ttc ctg gga gta ggc ctt 48
 Ile Gly Leu Leu Cys Gly Val Ala Phe Cys Phe Leu Gly Val Gly Leu
 1 5 10 15
 ttg aac gca caa gtg act caa acc ccg aga caa ctc atc aaa aaa gtg 96
 Leu Asn Ala Gln Val Thr Gln Thr Pro Arg Gln Leu Ile Lys Lys Val
 20 25 30
 gga gcg aaa gtt ttg ttg aaa tgt tca cag aat atg gac cat gaa aga 144
 Gly Ala Lys Val Leu Leu Lys Cys Ser Gln Asn Met Asp His Glu Arg
 35 40 45
 atg ttc tgg tat cga caa gac cca ggt ctg ggg ttg cgg ctg ctc tac 192
 Met Phe Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Leu Leu Tyr
 50 55 60
 tgg tcc tat aat att gac agt gtt gag aca gga gac atc cct tat ggg 240
 Trp Ser Tyr Asn Ile Asp Ser Val Glu Thr Gly Asp Ile Pro Tyr Gly
 65 70 75 80
 tac agt gtc tcg agg aag aag aag gat gcc ttc ccc ttg att ctg gag 288
 Tyr Ser Val Ser Arg Lys Lys Lys Asp Ala Phe Pro Leu Ile Leu Glu
 85 90 95
 tct gct cgc atc aac cag aca tct gtg tac ttc tgc gcc agc agc 333
 Ser Ala Arg Ile Asn Gln Thr Ser Val Tyr Phe Cys Ala Ser Ser
 100 105 110

<210> 29

<211> 111

<212> PRT

<213> Canis familiaris

<400> 29

Ile Gly Leu Leu Cys Gly Val Ala Phe Cys Phe Leu Gly Val Gly Leu
 1 5 10 15

Leu Asn Ala Gln Val Thr Gln Thr Pro Arg Gln Leu Ile Lys Lys Val
 20 25 30

Gly Ala Lys Val Leu Leu Lys Cys Ser Gln Asn Met Asp His Glu Arg
 35 40 45

Met Phe Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Leu Leu Tyr
 50 55 60

Trp Ser Tyr Asn Ile Asp Ser Val Glu Thr Gly Asp Ile Pro Tyr Gly
 65 70 75 80

Tyr Ser Val Ser Arg Lys Lys Lys Asp Ala Phe Pro Leu Ile Leu Glu
 85 90 95

Ser Ala Arg Ile Asn Gln Thr Ser Val Tyr Phe Cys Ala Ser Ser
 100 105 110

<210> 30

<211> 333

<212> DNA

<213> Canis familiaris

<400> 30

gctactggcg cagaagtaca cagatgtctg gttgatgcga gcagactcca gaatcaagg 60
 gaaggcatcc ttcttcttcc tcgagacact gtaccataa gggatgtctc ctgtctcaac 120
 actgtcaata ttataggacc agtagagcag ccgcaacccc agacctgggt cttgtcgata 180
 ccagaacatt ctttcatggg ccatattctg tgaacatttc aacaaaactt tcgctccac 240
 ttttttgatg agttgtctcg gggtttgagt cacttgtgcg ttcaaaaggc ctactcccag 300
 gaaacaaaag gccacaccac agaggagtcc gat 333

<210> 31

<211> 351

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (25)..(351)

<400> 31

acggtgaagg gctagcacct aaag atg ctg act tgc ctg cta ctc ctc ctg 51
 Met Leu Thr Cys Leu Leu Leu Leu
 1 5

gga caa ggc tct gtg ttt gga gct ctt gtc tct caa aag ccg cgc agg 99
 Gly Gln Gly Ser Val Phe Gly Ala Leu Val Ser Gln Lys Pro Arg Arg
 10 15 20 25

gac atc tgt caa cgt ggg acc tcc att acc atc cac tgt gag gtc gat 147
 Asp Ile Cys Gln Arg Gly Thr Ser Ile Thr Ile His Cys Glu Val Asp
 30 35 40

acc caa gtc acc ttg atg ttc tgg tac cgt cag ctc cca gga cag agc 195
 Thr Gln Val Thr Leu Met Phe Trp Tyr Arg Gln Leu Pro Gly Gln Ser
 45 50 55

ttg ata ctg att gca acc gca aac cag ggt gca gag gcc acc tac gaa 243
 Leu Ile Leu Ile Ala Thr Ala Asn Gln Gly Ala Glu Ala Thr Tyr Glu
 60 65 70

agt gga ttt acc agg gag aag ttt ccc atc agc cgc cga acc cta atg 291
 Ser Gly Phe Thr Arg Glu Lys Phe Pro Ile Ser Arg Arg Thr Leu Met
 75 80 85

ttc tcc act ctg act gtg agc aac ctg agc ctc gaa gac acc agc tct 339
 Phe Ser Thr Leu Thr Val Ser Asn Leu Ser Leu Glu Asp Thr Ser Ser
 90 95 100 105

tac ttc tgc agc 351
 Tyr Phe Cys Ser

<210> 32

<211> 109

<212> PRT

<213> Canis familiaris

<400> 32

Met Leu Thr Cys Leu Leu Leu Leu Leu Gly Gln Gly Ser Val Phe Gly
 1 5 10 15

Ala Leu Val Ser Gln Lys Pro Arg Arg Asp Ile Cys Gln Arg Gly Thr
 20 25 30

Ser Ile Thr Ile His Cys Glu Val Asp Thr Gln Val Thr Leu Met Phe

35 40 45
 Trp Tyr Arg Gln Leu Pro Gly Gln Ser Leu Ile Leu Ile Ala Thr Ala
 50 55 60
 Asn Gln Gly Ala Glu Ala Thr Tyr Glu Ser Gly Phe Thr Arg Glu Lys
 65 70 75 80
 Phe Pro Ile Ser Arg Arg Thr Leu Met Phe Ser Thr Leu Thr Val Ser
 85 90 95
 Asn Leu Ser Leu Glu Asp Thr Ser Ser Tyr Phe Cys Ser
 100 105

<210> 33
 <211> 351
 <212> DNA
 <213> Canis familiaris

<400> 33
 gctgcagaag taagagctgg tgtcttcgag gctcaggtg ctcacagtca gaggaggagaa 60
 cattaggggtt cggcggtga tgggaaactt ctccctggta aatccacttt cgtaggtggc 120
 ctctgcaccc tggtttgagg ttgcaatcag tatcaagctc tgcctggga gctgacggta 180
 ccagaacatc aagggtgactt gggatatgac ctcacagtgg atggtaatgg aggtcccacg 240
 ttgacagatg tccttgccgg gcttttgaga gacaagagct ccaaacacag agccttgctc 300
 caggaggagt agcaggcaag tcagcatctt taggtgctag cccttcaccg t 351

<210> 34
 <211> 339
 <212> DNA
 <213> Canis familiaris

<220>
 <221> CDS
 <222> (7)..(339)

<400> 34
 gctgaa atg gcc acc ggc gtc ttc ttt ggc atg gct ctt tgt gtc ctg 48
 Met Ala Thr Gly Val Phe Phe Gly Met Ala Leu Cys Val Leu
 1 5 10
 tgg aca gga tac atg gat gct gga att atc cag agc cca aga tac aag 96
 Trp Thr Gly Tyr Met Asp Ala Gly Ile Ile Gln Ser Pro Arg Tyr Lys
 15 20 25 30

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gtc aca ggg aca gga aag agg gtg act ctg aga tgt cac cag aca gac 144
Val Thr Gly Thr Gly Lys Arg Val Thr Leu Arg Cys His Gln Thr Asp
          35                      40                      45

aac tat gac tat atg tac tgg tat cga cat gac ctg gga cat ggg ccg 192
Asn Tyr Asp Tyr Met Tyr Trp Tyr Arg His Asp Leu Gly His Gly Pro
          50                      55                      60

agg ctg atc tat tat tca aat ggt att aac agc act gaa aaa gga gac 240
Arg Leu Ile Tyr Tyr Ser Asn Gly Ile Asn Ser Thr Glu Lys Gly Asp
          65                      70                      75

ctc tcc aat gga tac aca gtc tct aga tca aac aag atg gat ttc ccc 288
Leu Ser Asn Gly Tyr Thr Val Ser Arg Ser Asn Lys Met Asp Phe Pro
          80                      85                      90

ctc cta ctg gac tct gtt acc tcc tcc cag aca tct gtg tac ttc tgt 336
Leu Leu Leu Asp Ser Val Thr Ser Ser Gln Thr Ser Val Tyr Phe Cys
          95                      100                      105                      110

gcc 339
Ala

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<210> 35
 <211> 111
 <212> PRT
 <213> Canis familiaris

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<400> 35
Met Ala Thr Gly Val Phe Phe Gly Met Ala Leu Cys Val Leu Trp Thr
  1          5          10          15

Gly Tyr Met Asp Ala Gly Ile Ile Gln Ser Pro Arg Tyr Lys Val Thr
  20          25          30

Gly Thr Gly Lys Arg Val Thr Leu Arg Cys His Gln Thr Asp Asn Tyr
  35          40          45

Asp Tyr Met Tyr Trp Tyr Arg His Asp Leu Gly His Gly Pro Arg Leu
  50          55          60

Ile Tyr Tyr Ser Asn Gly Ile Asn Ser Thr Glu Lys Gly Asp Leu Ser
  65          70          75          80

Asn Gly Tyr Thr Val Ser Arg Ser Asn Lys Met Asp Phe Pro Leu Leu
          85          90          95

Leu Asp Ser Val Thr Ser Ser Gln Thr Ser Val Tyr Phe Cys Ala
  100          105          110

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<210> 36

<211> 339

<212> DNA

<213> Canis familiaris

<400> 36

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ggcacagaag tacacagatg tctgggagga ggtaacagag tccagtagga ggggggaaatc 60
catcttgttt gatctagaga ctgtgtatcc attggagagg tctccttttt cagtgtgtgt 120
aataccattt gaataataga tcagcctcgg cccatgtccc aggtcatgtc gataccagta 180
catatagtca tagttgtctg tctgggtgaca tctcagagtc accctctttc ctgtccctgt 240
gaccttgtagt cttgggctct ggataattcc agcatccatg tatcctgtcc acaggacaca 300
aagagccatg ccaaagaaga cgccgggtggc catttcagc                               339

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<210> 37

<211> 423

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (85)..(423)

<400> 37

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aattaaccct cactaaaggg aacaaaagct ggagctccac cgcggcacga ggagcgggga 60
ggctatcagc ttcccagggc tgcc atg ggc tcc agg ctt ctc tgc tgt gtg      111
                               Met Gly Ser Arg Leu Leu Cys Cys Val
                               1                               5

gcc ctt tgt ctc ctg gga gcc ggc ccc gtg gag tct gag gtc atc caa      159
Ala Leu Cys Leu Leu Gly Ala Gly Pro Val Glu Ser Glu Val Ile Gln
 10                               15                               20                               25

act cca aga cac atg atc aaa gca aga gga cag aca gtg acc ctg aga      207
Thr Pro Arg His Met Ile Lys Ala Arg Gly Gln Thr Val Thr Leu Arg
                               30                               35                               40

tgt tcc ctt atc tct gga cac cta tct gtg tac tgg tac caa cag gcc      255
Cys Ser Leu Ile Ser Gly His Leu Ser Val Tyr Trp Tyr Gln Gln Ala
                               45                               50                               55

ctg ggc cag ggt ccc cgg ttt ctc att cag tat tac aat agg gaa gag      303
Leu Gly Gln Gly Pro Arg Phe Leu Ile Gln Tyr Tyr Asn Arg Glu Glu
 60                               65                               70

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aga gac aaa gga gac atc ccg gca aga ttc tca gtg cag cag ttc agt 351
 Arg Asp Lys Gly Asp Ile Pro Ala Arg Phe Ser Val Gln Gln Phe Ser
 75 80 85

aac tac agc tcc cag ctg gag atg aac tcc ctg gag cca gga gac tca 399
 Asn Tyr Ser Ser Gln Leu Glu Met Asn Ser Leu Glu Pro Gly Asp Ser
 90 95 100 105

gcc cta tat ctc tgt gcc agc agc 423
 Ala Leu Tyr Leu Cys Ala Ser Ser
 110

<210> 38
 <211> 113
 <212> PRT
 <213> Canis familiaris

<400> 38
 Met Gly Ser Arg Leu Leu Cys Cys Val Ala Leu Cys Leu Leu Gly Ala
 1 5 10 15

Gly Pro Val Glu Ser Glu Val Ile Gln Thr Pro Arg His Met Ile Lys
 20 25 30

Ala Arg Gly Gln Thr Val Thr Leu Arg Cys Ser Leu Ile Ser Gly His
 35 40 45

Leu Ser Val Tyr Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Arg Phe
 50 55 60

Leu Ile Gln Tyr Tyr Asn Arg Glu Glu Arg Asp Lys Gly Asp Ile Pro
 65 70 75 80

Ala Arg Phe Ser Val Gln Gln Phe Ser Asn Tyr Ser Ser Gln Leu Glu
 85 90 95

Met Asn Ser Leu Glu Pro Gly Asp Ser Ala Leu Tyr Leu Cys Ala Ser
 100 105 110

Ser

<210> 39
 <211> 423
 <212> DNA
 <213> Canis familiaris

<400> 39
 gctgctggca cagagatata gggctgagtc tcttggtcc agggagttca tctccagctg 60

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<210> 40
<211> 396
<212> DNA
<213> Canis familiaris
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<220>  
<221> CDS  
<222> (73) .. (396)
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<400> 40																		
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catcacctga ag atg ctg atg ctt ctg ctg ctc ctg ggg ccc agc tct gga																		111
Met Leu Met Leu Leu Leu Leu Leu Gly Pro Ser Ser Gly																		
1 5 10																		
ctc ggt gcc ctc gtc ttc cag gcg ccc agc aca atg atc tgt aag agc																		159
Leu Gly Ala Leu Val Phe Gln Ala Pro Ser Thr Met Ile Cys Lys Ser																		
15 20 25																		
gga gcc acc gtg cag atc cag tgt caa aca gtg gac ctt caa gcc aca																		207
Gly Ala Thr Val Gln Ile Gln Cys Gln Thr Val Asp Leu Gln Ala Thr																		
30 35 40 45																		
acc gtg ttt tgg tat cgc cag ctc ccg aag cag ggc ctt acc ctt atg																		255
Thr Val Phe Trp Tyr Arg Gln Leu Pro Lys Gln Gly Leu Thr Leu Met																		
50 55 60																		
gtg acc tct aac gtg ggc aac agt gct aca cac gag cag ggg ttc cct																		303
Val Thr Ser Asn Val Gly Asn Ser Ala Thr His Glu Gln Gly Phe Pro																		
65 70 75																		
gca gcc aag ttc cct gtt aac cac cca aac ctc acg ttt tcc tcc ctg																		351
Ala Ala Lys Phe Pro Val Asn His Pro Asn Leu Thr Phe Ser Ser Leu																		
80 85 90																		

atg gtg acg agt tca ggt cct gga gac agc ggc ctc tac ttc tgt 396
 Met Val Thr Ser Ser Gly Pro Gly Asp Ser Gly Leu Tyr Phe Cys
 95 100 105

<210> 41
 <211> 108
 <212> PRT
 <213> Canis familiaris

<400> 41
 Met Leu Met Leu Leu Leu Leu Leu Gly Pro Ser Ser Gly Leu Gly Ala
 1 5 10 15
 Leu Val Phe Gln Ala Pro Ser Thr Met Ile Cys Lys Ser Gly Ala Thr
 20 25 30
 Val Gln Ile Gln Cys Gln Thr Val Asp Leu Gln Ala Thr Thr Val Phe
 35 40 45
 Trp Tyr Arg Gln Leu Pro Lys Gln Gly Leu Thr Leu Met Val Thr Ser
 50 55 60
 Asn Val Gly Asn Ser Ala Thr His Glu Gln Gly Phe Pro Ala Ala Lys
 65 70 75 80
 Phe Pro Val Asn His Pro Asn Leu Thr Phe Ser Ser Leu Met Val Thr
 85 90 95
 Ser Ser Gly Pro Gly Asp Ser Gly Leu Tyr Phe Cys
 100 105

<210> 42
 <211> 396
 <212> DNA
 <213> Canis familiaris

<400> 42
 acagaagtag aggccgctgt ctccaggacc tgaactcgtc accatcaggg aggaaaacgt 60
 gaggtttggg tggttaacag ggaacttggc tgcagggaa cctgctcgt gtgtagcact 120
 gttgcccacg ttagagggtca ccataagggt aaggccctgc ttcgggagct ggcgatacca 180
 aaacacgggt gtggcttgaa ggtccactgt ttgacactgg atctgcacgg tggctccgct 240
 cttacagatc attgtgctgg gcgcctggaa gacgagggca ccgagtccag agctgggccc 300
 caggagcagc agaagcatca gcattctcag gtgatggcct cataccatac ctctctcaag 360

atagatatga ccacgcctcg tgccgaatcc tgcagc

396

<210> 43

<211> 354

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (13)..(354)

<400> 43

cacgagcctg cc atg tgc cca gtg ttc atc tgc tcc ttg gtc ctc tgg ctc 51
Met Cys Pro Val Phe Ile Cys Ser Leu Val Leu Trp Leu
1 5 10

ctg agt aca ggc acc ctc aat gca aaa gtc atg cag act cca gga cat 99
Leu Ser Thr Gly Thr Leu Asn Ala Lys Val Met Gln Thr Pro Gly His
15 20 25

ctg gtc aaa ggg aaa gga caa aaa gca aaa atg gaa tgt gtc cca ata 147
Leu Val Lys Gly Lys Gly Gln Lys Ala Lys Met Glu Cys Val Pro Ile
30 35 40 45

aaa gga cat agt tat gtt ttc tgg tat cag cag atc cca gca aaa gag 195
Lys Gly His Ser Tyr Val Phe Trp Tyr Gln Gln Ile Pro Ala Lys Glu
50 55 60

ttc aag ttc ttg att tct ttc cag gat aac gct gtc ttt gat aaa aca 243
Phe Lys Phe Leu Ile Ser Phe Gln Asp Asn Ala Val Phe Asp Lys Thr
65 70 75

ggg atg ccc acg cag aga ttt tta gcc ttg tgt cca aaa aac cta ccc 291
Gly Met Pro Thr Gln Arg Phe Leu Ala Leu Cys Pro Lys Asn Leu Pro
80 85 90

tgt agc cta gag atc gag cgt aca gag ctg cag gat tca gcc gtg tat 339
Cys Ser Leu Glu Ile Glu Arg Thr Glu Leu Gln Asp Ser Ala Val Tyr
95 100 105

ttt tgt gcc agc agt 354
Phe Cys Ala Ser Ser
110

<210> 44

<211> 114

<212> PRT

<213> Canis familiaris

<400> 44

Met Cys Pro Val Phe Ile Cys Ser Leu Val Leu Trp Leu Leu Ser Thr
 1 5 10 15

Gly Thr Leu Asn Ala Lys Val Met Gln Thr Pro Gly His Leu Val Lys
 20 25 30

Gly Lys Gly Gln Lys Ala Lys Met Glu Cys Val Pro Ile Lys Gly His
 35 40 45

Ser Tyr Val Phe Trp Tyr Gln Gln Ile Pro Ala Lys Glu Phe Lys Phe
 50 55 60

Leu Ile Ser Phe Gln Asp Asn Ala Val Phe Asp Lys Thr Gly Met Pro
 65 70 75 80

Thr Gln Arg Phe Leu Ala Leu Cys Pro Lys Asn Leu Pro Cys Ser Leu
 85 90 95

Glu Ile Glu Arg Thr Glu Leu Gln Asp Ser Ala Val Tyr Phe Cys Ala
 100 105 110

Ser Ser

<210> 45

<211> 354

<212> DNA

<213> Canis familiaris

<400> 45

actgctggca caaaaataca cggctgaatc ctgcagctct gtacgctcga tctctaggct 60
 acagggtagg ttttttggac acaaggctaa aaatctctgc gtgggcatcc ctgttttata 120
 aaagacagcg ttatcctgga aagaaatcaa gaacttgaac tcttttgctg ggatctgctg 180
 ataccagaaa acataactat gtccttttat tgggacacat tccatttttg ctttttgtec 240
 tttccctttg accagatgtc ctggagtctg catgaacttt gcattgaggg tgctgtact 300
 caggagccag aggaccaagg agcagatgaa cactgggcac atggcaggct cgtg 354

<210> 46

<211> 369

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (40)..(369)

<400> 46

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ggcaccgagca ctgaggacca gactgtgcct gtctccacc atg ggc tcc ggg ttc      54
                                   Met Gly Ser Gly Phe
                                   1           5

ctc tgc tgt atg gtc ctc tgc ctc ctg gga gca gca ccc ctg gac aca      102
Leu Cys Cys Met Val Leu Cys Leu Leu Gly Ala Ala Pro Leu Asp Thr
              10              15              20

aca gtt tcc cag act cca aga tac ctc atc gcg cac gtg gga tcg aag      150
Thr Val Ser Gln Thr Pro Arg Tyr Leu Ile Ala His Val Gly Ser Lys
              25              30              35

aag tta cta aaa tgt gag caa aat ctg ggc cat aat gct atg tac tgg      198
Lys Leu Leu Lys Cys Glu Gln Asn Leu Gly His Asn Ala Met Tyr Trp
              40              45              50

tat aag caa gac ctc aag caa ctg ctg aag atc atg ttt atc tac ttt      246
Tyr Lys Gln Asp Leu Lys Gln Leu Leu Lys Ile Met Phe Ile Tyr Phe
              55              60              65

aat cag gga ctc aat cta aat gaa tca gtt cca ggt cgt ttc tca cct      294
Asn Gln Gly Leu Asn Leu Asn Glu Ser Val Pro Gly Arg Phe Ser Pro
              70              75              80              85

gag aca ctg aca agc tca tta act tca tgt cga ctc ctg aac agt gac      342
Glu Thr Leu Thr Ser Ser Leu Thr Ser Cys Arg Leu Leu Asn Ser Asp
              90              95              100

tct gct gtg tat ttc tgt gcc agc agc      369
Ser Ala Val Tyr Phe Cys Ala Ser Ser
              105              110

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<210> 47

<211> 110

<212> PRT

<213> Canis familiaris

<400> 47

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Met Gly Ser Gly Phe Leu Cys Cys Met Val Leu Cys Leu Leu Gly Ala
  1           5           10           15

Ala Pro Leu Asp Thr Thr Val Ser Gln Thr Pro Arg Tyr Leu Ile Ala
  20           25           30

His Val Gly Ser Lys Lys Leu Leu Lys Cys Glu Gln Asn Leu Gly His
  35           40           45

```

Asn Ala Met Tyr Trp Tyr Lys Gln Asp Leu Lys Gln Leu Leu Lys Ile
 50 55 60
 Met Phe Ile Tyr Phe Asn Gln Gly Leu Asn Leu Asn Glu Ser Val Pro
 65 70 75 80
 Gly Arg Phe Ser Pro Glu Thr Leu Thr Ser Ser Leu Thr Ser Cys Arg
 85 90 95
 Leu Leu Asn Ser Asp Ser Ala Val Tyr Phe Cys Ala Ser Ser
 100 105 110

<210> 48
 <211> 369
 <212> DNA
 <213> Canis familiaris

<400> 48
 gctgctggca cagaaatata cagcagagtc actgttcagg agtcgacatg aagttaatga 60
 gcttgctcagt gtctcagggtg agaaacgacc tggaactgat tcatttagat tgagtccttg 120
 attaaagtag ataaacatga tcttcagcag ttgcttgagg tcttgcttat accagtacat 180
 agcattatgg cccagatttt gctcacattt tagtaacttc ttcgatccca cgtgcgcgat 240
 gaggtatctt ggagtcctggg aaactgttgt gtccaggggt gctgctccca ggaggcagag 300
 gaccatacag cagaggaacc cggagcccat ggtggagaca ggcacagtct ggtcctcagt 360
 gctcgtgcc 369

<210> 49
 <211> 504
 <212> DNA
 <213> Canis familiaris

<400> 49
 gaggatctgc agaaggtcac cctccccacg gtcacagtgt ttgaaccatc ggaagcagag 60
 atctcgcgga cccagaaggc cacactcgtg tgcttgcca cgggcttcta ccccgaccac 120
 gtggagctga gctggtgggt gaacgggaag gaggtcacga gtgggttcag caccgacccg 180
 cagccctaca aggagaggcc cagcgagaat gactccagct actgtctgag cagccggctg 240
 agggctctctg cctccttctg gcacaacccg cgcaaccact tccgctgcca agtccagttc 300
 tatgggctcg gggacgacga tgagtggaaa tacgatagag tcaaaccat caccagaaac 360

atcagtgctg aggctgggg cagagcagac tgtggcttca cctcggtgtc ctaccatcag 420
ggcgctcctgt ctgccaccat cctctatgag atcctgctgg gcaaggccac gctgtatgct 480
gtgctgggtca gcatcctggt gctg 504

<210> 50
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 50
cgacaagacc caggtctgg 19

<210> 51
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 51
gtcagctccc aggacagag 19

<210> 52
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 52
catgacctgg gacatgggc 19

<210> 53
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 53

gagatgttcc cttatctctg g

21

<210> 54

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 54

cctctaacgt gggcaacag

19

<210> 55

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 55

tcagcagatc ccagcaaaag

20

<210> 56

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 56

agcaagacct caagcaactg

20

<210> 57

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 57

gtgaccttct gcagatcctc

20

<210> 58

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 58

agctcagctc cacgtggtc

19

<210> 59

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 59

tgctgaaccc actcgtgac

19

<210> 60

<211> 109

<212> PRT

<213> Canis familiaris

<220>

<223> At location 109, Xaa = Ala or Ser

<400> 60

Ile Gly Leu Leu Cys Gly Val Ala Phe Cys Phe Leu Gly Val Gly Leu
1 5 10 15Leu Asn Ala Gln Val Thr Gln Thr Pro Arg Gln Leu Ile Lys Lys Val
20 25 30

Gly Arg Lys Val Leu Leu Lys Cys Ser Gln Asn Met Asp His Glu Arg
 35 40 45
 Trp Ser Tyr Asn Ile Asp Ser Val Glu Thr Gly Asp Ile Pro Tyr Gly
 50 55 60
 Met Phe Trp Tyr Gln Gln Asp Pro Gly Leu Gly Leu Arg Leu Leu Tyr
 65 70 75 80
 Tyr Ser Val Ser Arg Lys Lys Lys Asp Ala Phe Pro Leu Ile Leu Glu
 85 90 95
 Ser Ala Arg Ile Asn Gln Thr Ser Val Tyr Phe Cys Xaa
 100 105

<210> 61
 <211> 110
 <212> PRT
 <213> Canis familiaris

<220>
 <223> At locations 109 and 110, Xaa =Ala or Ser

<400> 61
 Ile Gly Leu Leu Cys Gly Val Ala Phe Cys Phe Leu Gly Val Gly Leu
 1 5 10 15

Leu Asn Ala Gln Val Thr Gln Thr Pro Arg Gln Leu Ile Lys Lys Val
 20 25 30

Gly Arg Lys Val Leu Leu Lys Cys Ser Gln Asn Met Asp His Glu Arg
 35 40 45

Trp Ser Tyr Asn Ile Asp Ser Val Glu Thr Gly Asp Ile Pro Tyr Gly
 50 55 60

Met Phe Trp Tyr Gln Gln Asp Pro Gly Leu Gly Leu Arg Leu Leu Tyr
 65 70 75 80

Tyr Ser Val Ser Arg Lys Lys Lys Asp Ala Phe Pro Leu Ile Leu Glu
 85 90 95

Ser Ala Arg Ile Asn Gln Thr Ser Val Tyr Phe Cys Xaa Xaa
 100 105 110

<210> 62
 <211> 111
 <212> PRT

<213> Canis familiaris

<220>

<223> At locations 109, 110 and 111, Xaa= Ala or Ser

<400> 62

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Ile Gly Leu Leu Cys Gly Val Ala Phe Cys Phe Leu Gly Val Gly Leu
 1             5             10             15
Leu Asn Ala Gln Val Thr Gln Thr Pro Arg Gln Leu Ile Lys Lys Val
      20             25             30
Gly Arg Lys Val Leu Leu Lys Cys Ser Gln Asn Met Asp His Glu Arg
      35             40             45
Trp Ser Tyr Asn Ile Asp Ser Val Glu Thr Gly Asp Ile Pro Tyr Gly
      50             55             60
Met Phe Trp Tyr Gln Gln Asp Pro Gly Leu Gly Leu Arg Leu Leu Tyr
      65             70             75             80
Tyr Ser Val Ser Arg Lys Lys Lys Asp Ala Phe Pro Leu Ile Leu Glu
      85             90             95
Ser Ala Arg Ile Asn Gln Thr Ser Val Tyr Phe Cys Xaa Xaa Xaa
      100            105            110

```

<210> 63

<211> 109

<212> PRT

<213> Canis familiaris

<220>

<223> At location 109, Xaa =Ala or Ser

<400> 63

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Met Leu Thr Cys Leu Leu Leu Leu Gly Gln Gly Ser Val Phe Gly
 1             5             10             15
Ala Leu Val Ser Gln Lys Pro Arg Arg Asp Ile Cys Gln Arg Gly Thr
      20             25             30
Ser Ile Thr Ile His Cys Glu Val Asp Thr Gln Val Thr Leu Met Phe
      35             40             45
Trp Tyr Arg Gln Leu Pro Gly Gln Ser Leu Ile Leu Ile Ala Thr Ala
      50             55             60
Ala Glu Ala Thr Tyr Glu Asn Gln Gly Ser Gly Phe Thr Arg Glu Lys
      65             70             75             80

```

Phe Pro Ile Ser Arg Arg Thr Leu Met Phe Ser Thr Leu Thr Val Ser
 85 90 95

Asn Leu Ser Leu Glu Asp Thr Ser Ser Tyr Phe Cys Xaa
 100 105

<210> 64

<211> 110

<212> PRT

<213> Canis familiaris

<220>

<223> At locations 109 and 110, Xaa = Ala or Ser

<400> 64

Met Leu Thr Cys Leu Leu Leu Leu Leu Gly Gln Gly Ser Val Phe Gly
 1 5 10 15

Ala Leu Val Ser Gln Lys Pro Arg Arg Asp Ile Cys Gln Arg Gly Thr
 20 25 30

Ser Ile Thr Ile His Cys Glu Val Asp Thr Gln Val Thr Leu Met Phe
 35 40 45

Trp Tyr Arg Gln Leu Pro Gly Gln Ser Leu Ile Leu Ile Ala Thr Ala
 50 55 60

Ala Glu Ala Thr Tyr Glu Asn Gln Gly Ser Gly Phe Thr Arg Glu Lys
 65 70 75 80

Phe Pro Ile Ser Arg Arg Thr Leu Met Phe Ser Thr Leu Thr Val Ser
 85 90 95

Asn Leu Ser Leu Glu Asp Thr Ser Ser Tyr Phe Cys Xaa Xaa
 100 105 110

<210> 65

<211> 111

<212> PRT

<213> Canis familiaris

<220>

<223> At locations 109, 110 and 111, Xaa =Ala or Ser

<400> 65

Met Leu Thr Cys Leu Leu Leu Leu Leu Gly Gln Gly Ser Val Phe Gly
 1 5 10 15

Ala Leu Val Ser Gln Lys Pro Arg Arg Asp Ile Cys Gln Arg Gly Thr
 20 25 30

Ser Ile Thr Ile His Cys Glu Val Asp Thr Gln Val Thr Leu Met Phe
 35 40 45

Trp Tyr Arg Gln Leu Pro Gly Gln Ser Leu Ile Leu Ile Ala Thr Ala
 50 55 60

Ala Glu Ala Thr Tyr Glu Asn Gln Gly Ser Gly Phe Thr Arg Glu Lys
 65 70 75 80

Phe Pro Ile Ser Arg Arg Thr Leu Met Phe Ser Thr Leu Thr Val Ser
 85 90 95

Asn Leu Ser Leu Glu Asp Thr Ser Ser Tyr Phe Cys Xaa Xaa Xaa
 100 105 110

<210> 66

<211> 111

<212> PRT

<213> Canis familiaris

<220>

<223> At location 111, Xaa = Ala or Ser

<400> 66

Met Ala Thr Gly Val Phe Phe Gly Met Ala Leu Cys Val Leu Trp Thr
 1 5 10 15

Gly Tyr Met Asp Ala Gly Ile Ile Gln Ser Pro Arg Tyr Lys Val Thr
 20 25 30

Gly Thr Gly Lys Arg Val Thr Leu Arg Cys His Gln Thr Asp Asn Tyr
 35 40 45

Asp Tyr Met Tyr Trp Tyr Arg His Asp Leu Gly His Gly Pro Arg Leu
 50 55 60

Ile Tyr Tyr Ser Asn Gly Ile Asn Ser Thr Glu Lys Gly Asp Leu Ser
 65 70 75 80

Asn Gly Tyr Thr Val Ser Arg Ser Asn Lys Met Asp Phe Pro Leu Leu
 85 90 95

Leu Asp Ser Val Thr Ser Ser Gln Thr Ser Val Tyr Phe Cys Xaa
 100 105 110

<210> 67

<211> 112

<212> PRT

<213> Canis familiaris

<220>

<223> At locations 111 and 112, Xaa = Ala or Ser

<400> 67

Met	Ala	Thr	Gly	Val	Phe	Phe	Gly	Met	Ala	Leu	Cys	Val	Leu	Trp	Thr
1				5					10					15	
Gly	Tyr	Met	Asp	Ala	Gly	Ile	Ile	Gln	Ser	Pro	Arg	Tyr	Lys	Val	Thr
			20					25					30		
Gly	Thr	Gly	Lys	Arg	Val	Thr	Leu	Arg	Cys	His	Gln	Thr	Asp	Asn	Tyr
		35					40					45			
Asp	Tyr	Met	Tyr	Trp	Tyr	Arg	His	Asp	Leu	Gly	His	Gly	Pro	Arg	Leu
	50					55					60				
Ile	Tyr	Tyr	Ser	Asn	Gly	Ile	Asn	Ser	Thr	Glu	Lys	Gly	Asp	Leu	Ser
65					70					75				80	
Asn	Gly	Tyr	Thr	Val	Ser	Arg	Ser	Asn	Lys	Met	Asp	Phe	Pro	Leu	Leu
				85					90					95	
Leu	Asp	Ser	Val	Thr	Ser	Ser	Gln	Thr	Ser	Val	Tyr	Phe	Cys	Xaa	Xaa
			100					105					110		

<210> 68

<211> 113

<212> PRT

<213> Canis familiaris

<220>

<223> At locations 111, 112 and 113, Xaa = Ala or Ser

<400> 68

Met	Ala	Thr	Gly	Val	Phe	Phe	Gly	Met	Ala	Leu	Cys	Val	Leu	Trp	Thr
1				5					10					15	
Gly	Tyr	Met	Asp	Ala	Gly	Ile	Ile	Gln	Ser	Pro	Arg	Tyr	Lys	Val	Thr
			20					25					30		
Gly	Thr	Gly	Lys	Arg	Val	Thr	Leu	Arg	Cys	His	Gln	Thr	Asp	Asn	Tyr
		35					40					45			
Asp	Tyr	Met	Tyr	Trp	Tyr	Arg	His	Asp	Leu	Gly	His	Gly	Pro	Arg	Leu
	50					55					60				
Ile	Tyr	Tyr	Ser	Asn	Gly	Ile	Asn	Ser	Thr	Glu	Lys	Gly	Asp	Leu	Ser
65					70					75				80	

Asn Gly Tyr Thr Val Ser Arg Ser Asn Lys Met Asp Phe Pro Leu Leu
 85 90 95

Leu Asp Ser Val Thr Ser Ser Gln Thr Ser Val Tyr Phe Cys Xaa Xaa
 100 105 110

Xaa

<210> 69

<211> 111

<212> PRT

<213> Canis familiaris

<220>

<223> At location 111, Xaa = Ala or Ser

<400> 69

Met Gly Ser Arg Leu Leu Cys Cys Val Ala Leu Cys Leu Leu Gly Ala
 1 5 10 15

Gly Pro Val Glu Ser Glu Val Ile Gln Thr Pro Arg His Met Ile Lys
 20 25 30

Ala Arg Gly Gln Thr Val Thr Leu Arg Cys Ser Leu Ile Ser Gly His
 35 40 45

Leu Ser Val Tyr Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Arg Phe
 50 55 60

Leu Ile Gln Tyr Tyr Asn Arg Glu Glu Arg Asp Lys Gly Asp Ile Pro
 65 70 75 80

Ala Arg Phe Ser Val Gln Gln Phe Ser Asn Tyr Ser Ser Gln Leu Glu
 85 90 95

Met Asn Ser Leu Glu Pro Gly Asp Ser Ala Leu Tyr Leu Cys Xaa
 100 105 110

<210> 70

<211> 112

<212> PRT

<213> Canis familiaris

<220>

<223> At locations 111 and 112, Xaa = Ala or Ser

<400> 70

Met Gly Ser Arg Leu Leu Cys Cys Val Ala Leu Cys Leu Leu Gly Ala

1	5	10	15
Gly Pro Val	Glu Ser Glu Val	Ile Gln Thr Pro Arg His	Met Ile Lys
	20	25	30
Ala Arg Gly	Gln Thr Val Thr Leu Arg Cys Ser	Leu Ile Ser Gly His	
	35	40	45
Leu Ser Val	Tyr Trp Tyr Gln Gln Ala Leu Gly	Gln Gly Pro Arg Phe	
	50	55	60
Leu Ile Gln	Tyr Tyr Asn Arg Glu Glu Arg Asp	Lys Gly Asp Ile Pro	
	65	70	75
Ala Arg Phe	Ser Val Gln Gln Phe Ser Asn Tyr Ser Ser	Gln Leu Glu	
	85	90	95
Met Asn Ser	Leu Glu Pro Gly Asp Ser Ala Leu Tyr Leu	Cys Xaa Xaa	
	100	105	110

<210> 71

<211> 113

<212> PRT

<213> Canis familiaris

<220>

<223> At locations 111, 112 and 113, Xaa = Ala or Ser

<400> 71

Met Gly Ser	Arg Leu Leu Cys Cys Val	Ala Leu Cys Leu Leu Gly Ala
1	5	10
15		
Gly Pro Val	Glu Ser Glu Val Ile Gln Thr Pro Arg His	Met Ile Lys
	20	25
30		
Ala Arg Gly	Gln Thr Val Thr Leu Arg Cys Ser	Leu Ile Ser Gly His
	35	40
45		
Leu Ser Val	Tyr Trp Tyr Gln Gln Ala Leu Gly	Gln Gly Pro Arg Phe
	50	55
60		
Leu Ile Gln	Tyr Tyr Asn Arg Glu Glu Arg Asp	Lys Gly Asp Ile Pro
	65	70
75		
Ala Arg Phe	Ser Val Gln Gln Phe Ser Asn Tyr Ser Ser	Gln Leu Glu
	85	90
95		
Met Asn Ser	Leu Glu Pro Gly Asp Ser Ala Leu Tyr Leu	Cys Xaa Xaa
	100	105
110		

Xaa

<210> 72
 <211> 109
 <212> PRT
 <213> Canis familiaris

<220>
 <223> At location 109, Xaa = Ala or Ser

<400> 72
 Met Leu Met Leu Leu Leu Leu Gly Pro Ser Ser Gly Leu Gly Ala
 1 5 10 15
 Leu Val Phe Gln Ala Pro Ser Thr Met Ile Cys Lys Ser Gly Ala Thr
 20 25 30
 Val Gln Ile Gln Cys Gln Thr Val Asp Leu Gln Ala Thr Thr Val Phe
 35 40 45
 Trp Tyr Arg Gln Leu Pro Lys Gln Gly Leu Thr Leu Met Val Thr Ser
 50 55 60
 Asn Val Gly Asn Ser Ala Thr His Glu Gln Gly Phe Pro Ala Ala Lys
 65 70 75 80
 Phe Pro Val Asn His Pro Asn Leu Thr Phe Ser Ser Leu Met Val Thr
 85 90 95
 Ser Ser Gly Pro Gly Asp Ser Gly Leu Tyr Phe Cys Xaa
 100 105

<210> 73
 <211> 110
 <212> PRT
 <213> Canis familiaris

<220>
 <223> At location 109 and 110, Xaa = Ala or Ser

<400> 73
 Met Leu Met Leu Leu Leu Leu Gly Pro Ser Ser Gly Leu Gly Ala
 1 5 10 15
 Leu Val Phe Gln Ala Pro Ser Thr Met Ile Cys Lys Ser Gly Ala Thr
 20 25 30
 Val Gln Ile Gln Cys Gln Thr Val Asp Leu Gln Ala Thr Thr Val Phe
 35 40 45

Trp Tyr Arg Gln Leu Pro Lys Gln Gly Leu Thr Leu Met Val Thr Ser
 50 55 60

Asn Val Gly Asn Ser Ala Thr His Glu Gln Gly Phe Pro Ala Ala Lys
 65 70 75 80

Phe Pro Val Asn His Pro Asn Leu Thr Phe Ser Ser Leu Met Val Thr
 85 90 95

Ser Ser Gly Pro Gly Asp Ser Gly Leu Tyr Phe Cys Xaa Xaa
 100 105 110

<210> 74

<211> 111

<212> PRT

<213> Canis familiaris

<220>

<223> At locations 109, 110 and 111, Xaa = Ala or Ser

<400> 74

Met Leu Met Leu Leu Leu Leu Gly Pro Ser Ser Gly Leu Gly Ala
 1 5 10 15

Leu Val Phe Gln Ala Pro Ser Thr Met Ile Cys Lys Ser Gly Ala Thr
 20 25 30

Val Gln Ile Gln Cys Gln Thr Val Asp Leu Gln Ala Thr Thr Val Phe
 35 40 45

Trp Tyr Arg Gln Leu Pro Lys Gln Gly Leu Thr Leu Met Val Thr Ser
 50 55 60

Asn Val Gly Asn Ser Ala Thr His Glu Gln Gly Phe Pro Ala Ala Lys
 65 70 75 80

Phe Pro Val Asn His Pro Asn Leu Thr Phe Ser Ser Leu Met Val Thr
 85 90 95

Ser Ser Gly Pro Gly Asp Ser Gly Leu Tyr Phe Cys Xaa Xaa Xaa
 100 105 110

<210> 75

<211> 112

<212> PRT

<213> Canis familiaris

<220>

<223> At location 112, Xaa = Ala or Ser

<400> 75

Met Cys Pro Val Phe Ile Cys Ser Leu Val Leu Trp Leu Leu Ser Thr
 1 5 10 15

Gly Thr Leu Asn Ala Lys Val Met Gln Thr Pro Gly His Leu Val Lys
 20 25 30

Gly Lys Gly Gln Lys Ala Lys Met Glu Cys Val Pro Ile Lys Gly His
 35 40 45

Ser Tyr Val Phe Trp Tyr Gln Gln Ile Pro Ala Lys Glu Phe Lys Phe
 50 55 60

Leu Ile Ser Phe Gln Asp Asn Ala Val Phe Asp Lys Thr Gly Met Pro
 65 70 75 80

Thr Gln Arg Phe Leu Ala Leu Cys Pro Lys Asn Leu Pro Cys Ser Leu
 85 90 95

Glu Ile Glu Arg Thr Glu Leu Gln Asp Ser Ala Val Tyr Phe Cys Xaa
 100 105 110

<210> 76

<211> 113

<212> PRT

<213> Canis familiaris

<220>

<223> At location 112 and 113, Xaa = Ala or Ser

<400> 76

Met Cys Pro Val Phe Ile Cys Ser Leu Val Leu Trp Leu Leu Ser Thr
 1 5 10 15

Gly Thr Leu Asn Ala Lys Val Met Gln Thr Pro Gly His Leu Val Lys
 20 25 30

Gly Lys Gly Gln Lys Ala Lys Met Glu Cys Val Pro Ile Lys Gly His
 35 40 45

Ser Tyr Val Phe Trp Tyr Gln Gln Ile Pro Ala Lys Glu Phe Lys Phe
 50 55 60

Leu Ile Ser Phe Gln Asp Asn Ala Val Phe Asp Lys Thr Gly Met Pro
 65 70 75 80

Thr Gln Arg Phe Leu Ala Leu Cys Pro Lys Asn Leu Pro Cys Ser Leu
 85 90 95

Glu Ile Glu Arg Thr Glu Leu Gln Asp Ser Ala Val Tyr Phe Cys Xaa

100

105

110

Xaa

<210> 77

<211> 114

<212> PRT

<213> Canis familiaris

<220>

<223> At location 112, 113 and 114, Xaa = Ala or Ser

<400> 77

Met	Cys	Pro	Val	Phe	Ile	Cys	Ser	Leu	Val	Leu	Trp	Leu	Leu	Ser	Thr
1				5					10					15	

Gly	Thr	Leu	Asn	Ala	Lys	Val	Met	Gln	Thr	Pro	Gly	His	Leu	Val	Lys
			20					25					30		

Gly	Lys	Gly	Gln	Lys	Ala	Lys	Met	Glu	Cys	Val	Pro	Ile	Lys	Gly	His
		35					40					45			

Ser	Tyr	Val	Phe	Trp	Tyr	Gln	Gln	Ile	Pro	Ala	Lys	Glu	Phe	Lys	Phe
	50					55					60				

Leu	Ile	Ser	Phe	Gln	Asp	Asn	Ala	Val	Phe	Asp	Lys	Thr	Gly	Met	Pro
65					70					75					80

Thr	Gln	Arg	Phe	Leu	Ala	Leu	Cys	Pro	Lys	Asn	Leu	Pro	Cys	Ser	Leu
				85						90				95	

Glu	Ile	Glu	Arg	Thr	Glu	Leu	Gln	Asp	Ser	Ala	Val	Tyr	Phe	Cys	Xaa
			100					105					110		

Xaa Xaa

<210> 78

<211> 108

<212> PRT

<213> Canis familiaris

<220>

<223> At location 108, Xaa = Ala or Ser

<400> 78

Met	Gly	Ser	Gly	Phe	Leu	Cys	Cys	Met	Val	Leu	Cys	Leu	Leu	Gly	Ala
1				5					10					15	

Ala	Pro	Leu	Asp	Thr	Thr	Val	Ser	Gln	Thr	Pro	Arg	Tyr	Leu	Ile	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

20 25 30
 His Val Gly Ser Lys Lys Leu Leu Lys Cys Glu Gln Asn Leu Gly His
 35 40 45
 Asn Ala Met Tyr Trp Tyr Lys Gln Asp Leu Lys Gln Leu Leu Lys Ile
 50 55 60
 Met Phe Ile Tyr Phe Asn Gln Gly Leu Asn Leu Asn Glu Ser Val Pro
 65 70 75 80
 Gly Arg Phe Ser Pro Glu Thr Leu Thr Ser Ser Leu Thr Ser Cys Arg
 85 90 95
 Leu Leu Asn Ser Asp Ser Ala Val Tyr Phe Cys Xaa
 100 105

<210> 79

<211> 109

<212> PRT

<213> Canis familiaris

<220>

<223> At locations 108 and 109, Xaa = Ala or Ser

<400> 79

Met Gly Ser Gly Phe Leu Cys Cys Met Val Leu Cys Leu Leu Gly Ala
 1 5 10 15
 Ala Pro Leu Asp Thr Thr Val Ser Gln Thr Pro Arg Tyr Leu Ile Ala
 20 25 30
 His Val Gly Ser Lys Lys Leu Leu Lys Cys Glu Gln Asn Leu Gly His
 35 40 45
 Asn Ala Met Tyr Trp Tyr Lys Gln Asp Leu Lys Gln Leu Leu Lys Ile
 50 55 60
 Met Phe Ile Tyr Phe Asn Gln Gly Leu Asn Leu Asn Glu Ser Val Pro
 65 70 75 80
 Gly Arg Phe Ser Pro Glu Thr Leu Thr Ser Ser Leu Thr Ser Cys Arg
 85 90 95
 Leu Leu Asn Ser Asp Ser Ala Val Tyr Phe Cys Xaa Xaa
 100 105

<210> 80

<211> 110
 <212> PRT
 <213> Canis familiaris

<220>

<223> At locations 108, 109 and 110, Xaa = Ala or Ser

<400> 80

Met Gly Ser Gly Phe Leu Cys Cys Met Val Leu Cys Leu Leu Gly Ala
 1 5 10 15

Ala Pro Leu Asp Thr Thr Val Ser Gln Thr Pro Arg Tyr Leu Ile Ala
 20 25 30

His Val Gly Ser Lys Lys Leu Leu Lys Cys Glu Gln Asn Leu Gly His
 35 40 45

Asn Ala Met Tyr Trp Tyr Lys Gln Asp Leu Lys Gln Leu Leu Lys Ile
 50 55 60

Met Phe Ile Tyr Phe Asn Gln Gly Leu Asn Leu Asn Glu Ser Val Pro
 65 70 75 80

Gly Arg Phe Ser Pro Glu Thr Leu Thr Ser Ser Leu Thr Ser Cys Arg
 85 90 95

Leu Leu Asn Ser Asp Ser Ala Val Tyr Phe Cys Xaa Xaa Xaa
 100 105 110

<210> 81
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 Primer

<220>

<223> Y = T or C , R = G or A, N = A, C, G, or T

<400> 81

ccgaattctg gtaycrnca

19

<210> 82
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

Primer

<220>

<223> R = G or A

<400> 82

cggatccgcr cartarta

18

<210> 83

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<220>

<223> R = G or A

<400> 83

cggatccgcr caraarta

18

<210> 84

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 84

ccagacctgg gtcttgctg

19

<210> 85

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 85

ctctgtcctg ggagctga

18

<210> 86
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 86
ttgtttgatc tagagactgt g

21

<210> 87
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 87
atcggactcc tctgtggtgt

20

<210> 88
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 88
acggtgaagg gctagcacct

20

<210> 89
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 89
gctgaaatgg ccaccggcgt

20

<210> 90
<211> 19
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 90
ctgttgccca cgtagagg

19

<210> 91
<211> 19
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 91
ttactgaact gctgcactg

19

<210> 92
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 92
gctgcaggat tcggcacgag

20

<210> 93
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 93
tacgactgtc agcttggtcc

20

<210> 94
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 94
cttttgctgg gatctgctga

20

<210> 95
<211> 19
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 95
cagttgctta ggtcttgct

19

<210> 96
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 96
cacgagcctg ccatgtgccc

20

<210> 97
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 97
ggcacgagca ctgaggacca

20

<210> 98
 <211> 438
 <212> DNA
 <213> Canis familiaris

<220>
 <221> CDS
 <222> (40)..(438)

<400> 98
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 Met Gly Ser Arg Leu
 1 5

ctc tgc tgt gtg gcc ctt tgt ctc ctg gga gcc ggc ccc gtg gag tct 102
 Leu Cys Cys Val Ala Leu Cys Leu Leu Gly Ala Gly Pro Val Glu Ser
 10 15 20

gag gtc atc caa act cca aga cac atg atc aaa gca aga gga cag aca 150
 Glu Val Ile Gln Thr Pro Arg His Met Ile Lys Ala Arg Gly Gln Thr
 25 30 35

gtg acc ctg aga tgt tcc ctt atc tct gga cac cta tct gtg tac tgg 198
 Val Thr Leu Arg Cys Ser Leu Ile Ser Gly His Leu Ser Val Tyr Trp
 40 45 50

tac caa cag gcc ctg ggc cag ggt ccc cgg ttt ctc att cag tat tac 246
 Tyr Gln Gln Ala Leu Gly Gln Gly Pro Arg Phe Leu Ile Gln Tyr Tyr
 55 60 65

aat agg gaa gag aga gac aaa gga gac atc ccg gca aga ttc tca gtg 294
 Asn Arg Glu Glu Arg Asp Lys Gly Asp Ile Pro Ala Arg Phe Ser Val
 70 75 80 85

cag cag ttc agt aac tac agc tcc cag ctg gag atg aac tcc ctg gag 342
 Gln Gln Phe Ser Asn Tyr Ser Ser Gln Leu Glu Met Asn Ser Leu Glu
 90 95 100

cca gga gac tca gcc cta tat ctc tgt gcc agc agc tta gat gcg ttc 390
 Pro Gly Asp Ser Ala Leu Tyr Leu Cys Ala Ser Ser Leu Asp Ala Phe
 105 110 115

gac gcg ggg cag ctg tac ttc ggg gcc ggt tcc aag ctg gcc gtg ctg 438
 Asp Ala Gly Gln Leu Tyr Phe Gly Ala Gly Ser Lys Leu Ala Val Leu
 120 125 130

<210> 99
 <211> 133
 <212> PRT
 <213> Canis familiaris

<400> 99

Met Gly Ser Arg Leu Leu Cys Cys Val Ala Leu Cys Leu Leu Gly Ala
 1 5 10 15

Gly Pro Val Glu Ser Glu Val Ile Gln Thr Pro Arg His Met Ile Lys
 20 25 30

Ala Arg Gly Gln Thr Val Thr Leu Arg Cys Ser Leu Ile Ser Gly His
 35 40 45

Leu Ser Val Tyr Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Arg Phe
 50 55 60

Leu Ile Gln Tyr Tyr Asn Arg Glu Glu Arg Asp Lys Gly Asp Ile Pro
 65 70 75 80

Ala Arg Phe Ser Val Gln Gln Phe Ser Asn Tyr Ser Ser Gln Leu Glu
 85 90 95

Met Asn Ser Leu Glu Pro Gly Asp Ser Ala Leu Tyr Leu Cys Ala Ser
 100 105 110

Ser Leu Asp Ala Phe Asp Ala Gly Gln Leu Tyr Phe Gly Ala Gly Ser
 115 120 125

Lys Leu Ala Val Leu
 130

<210> 100

<211> 438

<212> DNA

<213> Canis familiaris

<400> 100

cagcacggcc agcttggaac cggccccgaa gtacagctgc cccgcgtcga acgcattctaa 60
 gctgctggca cagagatata gggctgagtc tcttggctcc agggagttca tctccagctg 120
 ggagctgtag ttactgaact gctgcactga gaatcttgcc gggatgtctc ctttgtctct 180
 ctcttcccta ttgtaatact gaatgagaaa ccggggaccc tggcccaggg cctgttggtta 240
 ccagtacaca gataggtgtc cagagataag ggaacatctc agggtcactg tctgtcctct 300
 tgctttgatc atgtgtcttg gagtttggat gacctcagac tccacggggc cggctcccag 360
 gagacaaagg gccacacagc agagaagcct ggagcccatg gcagccctgg gaagctgata 420
 gcctccccgc tctcgtg 438

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 99/17309

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/12 C12N15/62 C12N5/10 C07K14/705 C07K16/28
 C12Q1/68 A61K38/17 A61K31/70 A61K48/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K C12Q A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	DATABASE GENBANK [Online] Accession No. AF082505, 6 January 1999 (1999-01-06) DREITZ M.J. & SIM G.K.: "T cell receptor beta chain hcvb3 (Canis familiaris)" XP002122470 the whole document	1-48
X	--- WO 92 12996 A (IMMUNE RESPONSE CORP INC) 6 August 1992 (1992-08-06) abstract figure 1 examples 1-13 claims 1-113 --- -/-	1-48



Further documents are listed in the continuation of box C.



Patent family members are listed in annex.

* Special categories of cited documents :

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

Z document member of the same patent family

Date of the actual completion of the international search

16 November 1999

Date of mailing of the international search report

06.03.00

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
 NL - 2280 HV Rijswijk
 Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
 Fax: (+31-70) 340-3016

Authorized officer

Galli, I

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>WEDDERBURN L.R. ET AL.: "In vivo clonal dominance and limited T-cell receptor usage in human CD4+ T-cell recognition of house dust mite allergens" PROC. NATL. ACAD. SCI. USA, vol. 90, September 1993 (1993-09), pages 8214-8218, XP002122467 the whole document -& DATABASE GENBANK [Online] Accession No. Z23040, 17 January 1995 (1995-01-17) WEDDERBURN: "T-cell antigen receptor beta chain" XP002122471 compare seq. IDs 1 and 50 with nt 31-381 and 173-191, respectively</p>	1-48
A	<p>TAKANO M. ET AL.: "Identification of dog T-cell receptor beta chain genes" IMMUNOGENETICS, vol. 40, 1994, page 246 XP002122468 cited in the application the whole document</p>	1-48
A	<p>ITO K. ET AL.: "Isolation and sequence analysis of cDNA for the dog T-cell receptor Tcr-alpha and Tcr-beta chains" IMMUNOGENETICS, vol. 38, 1993, pages 60-63, XP002122469 cited in the application the whole document</p>	1-48
A	<p>US 5 635 354 A (KOURILSKY PHILIPPE ET AL) 3 June 1997 (1997-06-03) abstract</p>	1-48

INTERNATIONAL SEARCH REPORT

national application No.

PCT/US 99/ 17309

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although claims 44,45
are directed to a method of treatment of the human/animal
body, the search has been carried out and based on the alleged
effects of the compound/composition.
2. ☒ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such
an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all
searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment
of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report
covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is
restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-48 partially

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: (1-48) - partially

Isolated nCaV-beta3 polypeptide (seq. IDs 2,29,60,61,62) and homologs.

Corresponding nucleic acids (seq. IDs 1,28) and their allelic variants, complementary DNAs (Seq. ID 3,30), and a unique primer (Seq. ID 50).

Methods to detect expansion of T cells, therapeutic compositions, antibodies,kits.. Uses of said materials in therapeutic, diagnostic and detection applications.

2. Claims: (1-48) - partially

Idem as subject matter 1, but limited to mCaV-beta4 (Seq. IDs 5,32,63,64,65; 4,31,7; 6,33,8; 51)

3. Claims: (1-48) - partially

Idem as subject matter 1, but limited to mCaV-beta12 (Seq. IDs 10,35,66,67,68; 9,34,12; 11,36,13; 52)

4. Claims: (1-48) - partially

Idem as subject matter 1, but limited to mCaV-beta72 (seq. IDs 15,38,69,70,71,99; 37,98,17; 39,100,18; 53)

5. Claims: (3,6-9,20-48) - partially

Idem as subject matter 1, but limited to mCaV-beta21 (seq. IDs 20,72,73,74; 19; 54)

6. Claims: (3,6-9,20-48) - partially

Idem as subject matter 1, but limited to mCaV-beta54 (seq. IDs 23,75,76,77; 22; 24; 55)

7. Claims: (3,6-9,20-48) - partially

Idem as subject matter 1, but limited to mCaV-beta182 (seq. IDs 26,78,79,80; 25; 27; 56).

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claim 9 (points i and vi) refer to mimetopes and inhibitors of the polypeptides without giving a true technical characterization. Moreover, no such compounds are defined in the characterization. In consequence, the scope of said claims is ambiguous and vague, and their subject-matter is not sufficiently disclosed and supported (Art. 5 and 6 PCT). No search can be carried out for such purely speculative claims whose wording is, in fact, a mere recitation of the results to be achieved.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 99/17309

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
WO 9212996 A		06-08-1992	AU 1271692 A	27-08-1992
			AU 694062 B	09-07-1998
			AU 7032796 A	16-01-1997
			CA 2101065 A	23-07-1992
			EP 0568623 A	10-11-1993
			EP 0722738 A	24-07-1996
			JP 6507384 T	25-08-1994
			NO 932631 A	21-09-1993
			US 5985552 A	16-11-1999

US 5635354 A		03-06-1997	FR 2671356 A	10-07-1992
			CA 2100167 A	10-07-1992
			DE 69204823 D	19-10-1995
			DE 69204823 T	02-05-1996
			EP 0566685 A	27-10-1993
			ES 2079181 T	01-01-1996
			WO 9212260 A	23-07-1992
			JP 6508262 T	22-09-1994
